



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Re Application of:

Enno KLUSSMAN et al.

Serial No.: 10/526,768

Examiner: SWOPE, Sheridan PhD

Group Art Unit: 1652

Filed: NOVEMBER 7, 2005

Confirmation Number: 6937

Title: **AKAP18 DELTA, A NOVEL SPLICING VARIANT OF A PROTEIN KINASE A ANCHOR PROTEIN AND THE USE OF THE SAME**

**SEQUENCE LISTING TRANSMITTAL**

**MAIL STOP AMENDMENT SEQUENCE**

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

Sir:

Please replace the current sequence listing with the accompanying paper and electronic sequence listing. The undersigned confirms that the paper and electronic forms are the same.

Respectfully submitted,

---

Anthony J. Zelano, Reg. No. 27,969  
Attorney for Applicant(s)

MILLEN, WHITE, ZELANO  
& BRANIGAN, P.C.

Arlington Courthouse Plaza 1, Suite 1400  
2200 Clarendon Boulevard  
Arlington, Virginia 22201  
Telephone: (703) 243-6333  
Facsimile: (703) 243-6410

Attorney Docket No.: **HERTIN-0001**

Date: June 6, 2008

## SEQUENCE LISTING



<110> KLUSSMANN, ENNO  
OKSCHE, ALEXANDER  
ROSENTHAL, WALTER  
<120> NEW SPLICING VARIANT OF A PROTEIN KINASE A ANCHOR PROTEIN AND USE THEREOF

<130> HERTIN-0001

<140> 10/526,768  
<141> 2005-11-07

<150> PCT/EP03/09892  
<151> 2003-09-05

<150> DE 102 44 072.7  
<151> 2002-09-06

<150> DE 103 06 085.5  
<151> 2003-02-07

<160> 6

<170> PatentIn Ver. 3.3

<210> 1  
<211> 1062  
<212> DNA  
<213> Homo sapiens

<400> 1  
atggagcgcc ccgcccgcggg agaaaatagat gccaataagt gtgatcattt atcaagagga 60  
gaggaaggga cggggggaccc ggagaccagg cctgttagtt ctctggcaga cctgcccgtt 120  
gctgcccgttag acattcaaga tgactgtgga ctccctgatg tacctcaagg aaatgtaccc 180  
caaggaaacc caaagagaag caaaagaaaat agaggcgaca ggaatgtatca cgtgaagaag 240  
aggaagaagg ccaagaaaaga ttatcaaccc aactattcc tgccatattcc aatcaccaac 300  
aaaaagattt cagcttggaaat taaagtcttgc caaaatttgcg tactgagaca ggataatcg 360  
ttgaccggaaat ccattggctcg cgacggctcc tttcacatca ccttgcttagt gatgcagcta 420  
ttaaaccaag atgaagtaaa cataggttacc gacgcgcctt tggaaactgaa gccgttcgtt 480  
gaggagatcc ttgagggggaa gcatctgact ttgccttcc acgggattgg cactttccaa 540  
ggtcaggtt gctttgtgaa gctggcagac ggagatcacg tcagtgccct cctggagata 600  
gcagagactg caaaaaggac atttcaggaa aaaggcatcc tggctggaga aagcagaact 660  
tttaaggctc acctgaccc ttatgaagctg tccaaagcac caatgctctg gaagaaggaa 720  
gtgagaaaaa tagagcctgg attgtatgag caatttatcg accacagatt tggagaagaa 780  
atactgtacc aaatagatct ctgctccatg ctgaagaaaa aacagagcaa tggttattac 840  
caactgcgact ctgcgtatcg gatcggtgag aaggaccgaa aggagcctga ggatgctgaa 900  
ctggctcaggc tcagtaagag gctggtgag aacgcccgtgc tcaaggctgt ccagcagttac 960  
ctagaagaga cacagaacaa aaagcagccg ggggaggggaa actccgtcaa agctgaggag  
1020  
ggagatcgga atggcgatgg cagtgataac aaccggaagt ga  
1062

<210> 2  
<211> 353  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Glu Arg Pro Ala Ala Gly Glu Ile Asp Ala Asn Lys Cys Asp His  
1 5 10 15

Leu Ser Arg Gly Glu Glu Gly Thr Gly Asp Leu Glu Thr Ser Pro Val  
20 25 30

Gly Ser Leu Ala Asp Leu Pro Phe Ala Ala Val Asp Ile Gln Asp Asp  
35 40 45

Cys Gly Leu Pro Asp Val Pro Gln Gly Asn Val Pro Gln Gly Asn Pro  
50 55 60

Lys Arg Ser Lys Glu Asn Arg Gly Asp Arg Asn Asp His Val Lys Lys  
65 70 75 80

Arg Lys Lys Ala Lys Lys Asp Tyr Gln Pro Asn Tyr Phe Leu Ser Ile  
85 90 95

Pro Ile Thr Asn Lys Lys Ile Thr Ala Gly Ile Lys Val Leu Gln Asn  
100 105 110

Ser Ile Leu Arg Gln Asp Asn Arg Leu Thr Lys Ala Met Val Gly Asp  
115 120 125

Gly Ser Phe His Ile Thr Leu Leu Val Met Gln Leu Leu Asn Glu Asp  
130 135 140

Glu Val Asn Ile Gly Thr Asp Ala Leu Leu Glu Leu Lys Pro Phe Val  
145 150 155 160

Glu Glu Ile Leu Glu Gly Lys His Leu Thr Leu Pro Phe His Gly Ile  
165 170 175

Gly Thr Phe Gln Gly Gln Val Gly Phe Val Lys Leu Ala Asp Gly Asp  
180 185 190

His Val Ser Ala Leu Leu Glu Ile Ala Glu Thr Ala Lys Arg Thr Phe  
195 200 205

Gln Glu Lys Gly Ile Leu Ala Gly Glu Ser Arg Thr Phe Lys Pro His  
210 215 220

Leu Thr Phe Met Lys Leu Ser Lys Ala Pro Met Leu Trp Lys Lys Gly  
225 230 235 240

Val Arg Lys Ile Glu Pro Gly Leu Tyr Glu Gln Phe Ile Asp His Arg  
245 250 255

Phe Gly Glu Glu Ile Leu Tyr Gln Ile Asp Leu Cys Ser Met Leu Lys  
260 265 270

Lys Lys Gln Ser Asn Gly Tyr Tyr His Cys Glu Ser Ser Ile Val Ile  
275 280 285

Gly Glu Lys Asp Arg Lys Glu Pro Glu Asp Ala Glu Leu Val Arg Leu  
290 295 300

Ser Lys Arg Leu Val Glu Asn Ala Val Leu Lys Ala Val Gln Gln Tyr  
305 310 315 320

Leu Glu Glu Thr Gln Asn Lys Glu Gln Pro Gly Glu Gly Asn Ser Val  
325 330 335

Lys Ala Glu Glu Gly Asp Arg Asn Gly Asp Gly Ser Asp Asn Asn Arg  
340 345 350

Lys

<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 3  
ctcgagctca agttcgaat tctgatggag cgccccgccc cggg 44

<210> 4  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 4  
ggcgaccgggt ggatccgggg cccgggttgtt atcactgccca tcgcc 45

<210> 5  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 5  
tcagatctcg agctcaagct tcgaattctg atgagccaca tccagatccc g 51

<210> 6  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 6  
gaccgggtgga tcccgggcct gcccgggtt gcccagat 38